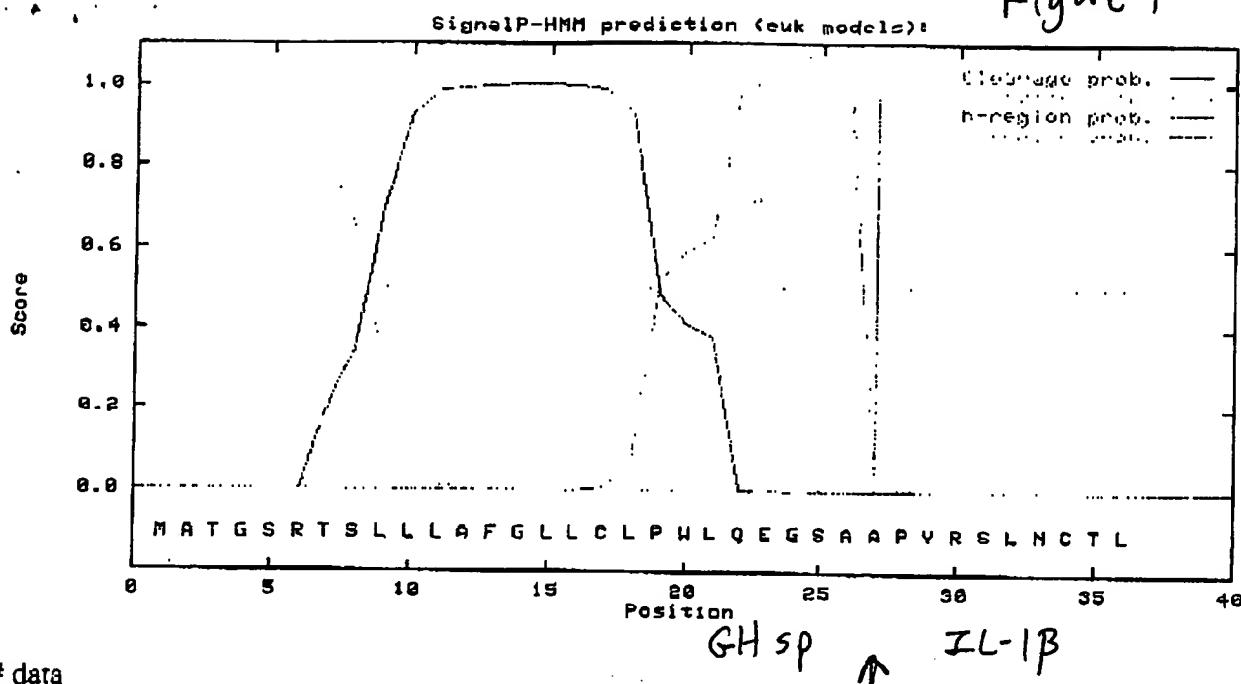


Figure 1



data

>#

Prediction: Signal peptide

Signal peptide probability: 1.000

Signal anchor probability: 0.000

Max cleavage site probability: 0.966 between pos. 26 and 27

gnuplot script for making the plot(s)

When using results from this server, please cite:

Henrik Nielsen, Jacob Englebrecht, Søren Brunak and Gunnar von Heijne: Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites. *Protein Engineering*, 10, 1-6 (1997).

If you specifically use the SignalP-HMM output, please also cite:

- Henrik Nielsen and Anders Krogh: Prediction of signal peptides and signal anchors by a hidden Markov model. In *Proceedings of the Sixth International Conference on Intelligent Systems for Molecular Biology (ISMB 6)*, AAAI Press. Menlo Park, California, pp. 122-130 (1998).

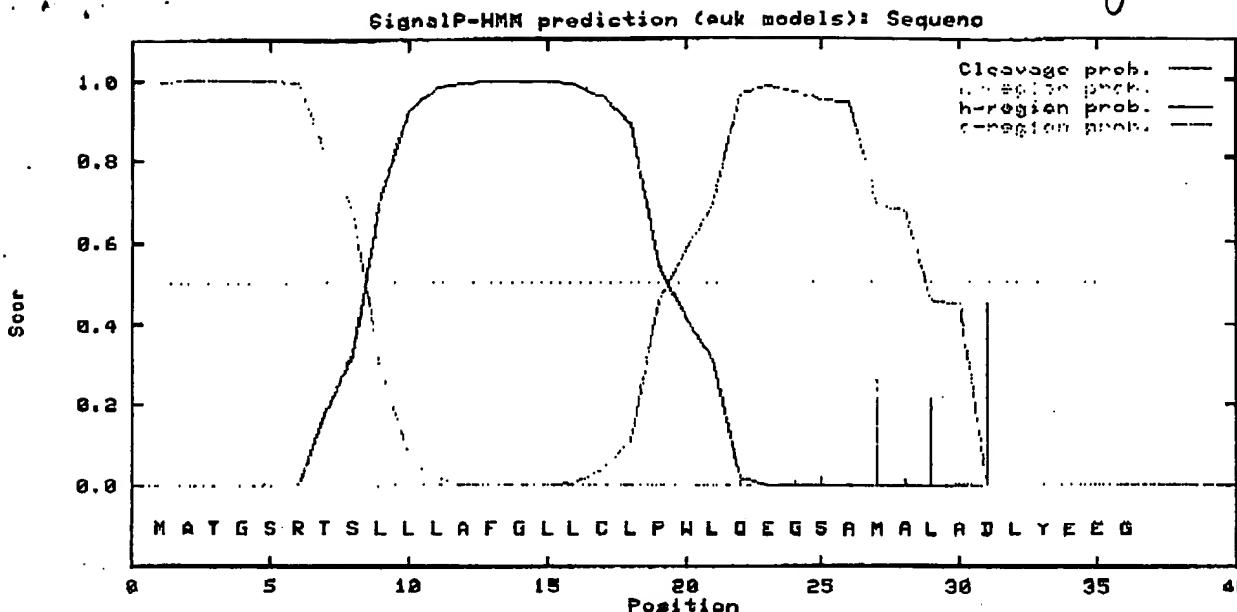
IL-1 β

GH sp

http://www.cbs.dtu.dk/cgi-bin/nph-webface?jobid=signalp_3F363F80022CDE6A&opt=none 8/10/2003



Figure 2



data

>Sequence

Prediction: Signal peptide

Signal peptide probability: 0.999

Signal anchor probability: 0.001

Max cleavage site probability: 0.450 between pos. 30 and 31

gnuplot script for making the plot(s)

When using results from this server, please cite:

- Henrik Nielsen, Jacob Engelbrecht, Søren Brunak and Gunnar von Heijne: Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites. *Protein Engineering*, 10, 1-6 (1997).

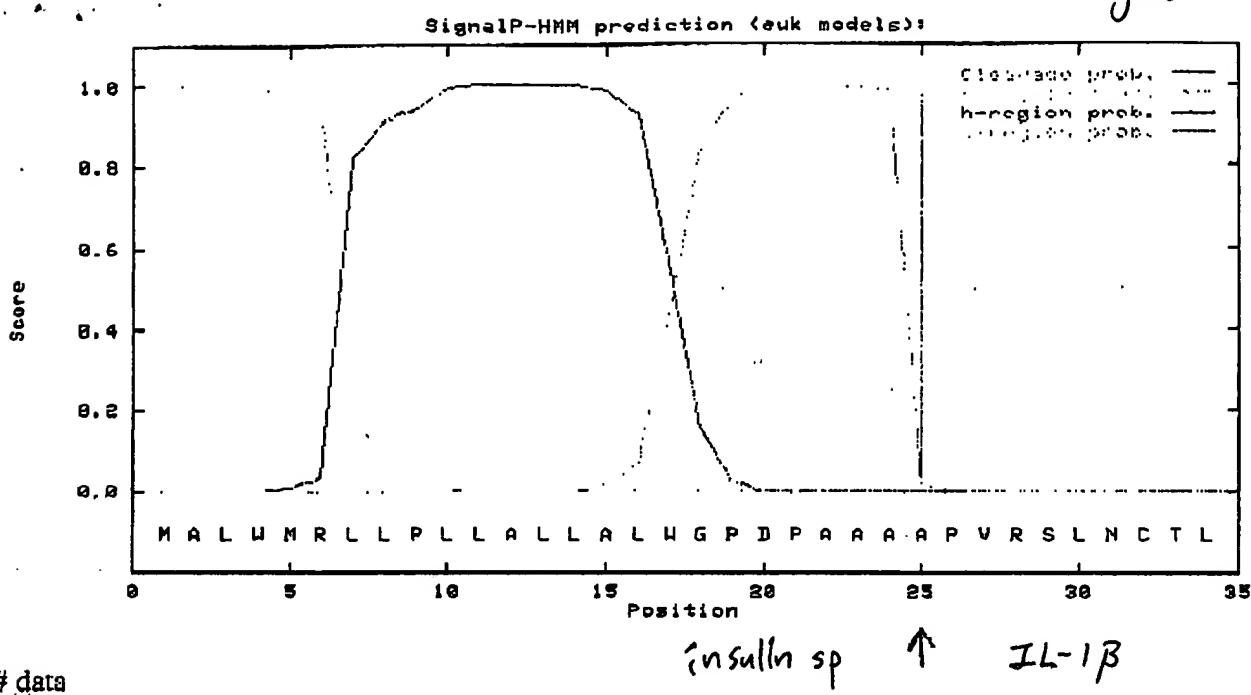
If you specifically use the SignalP-HMM output, please also cite:

- Henrik Nielsen and Anders Krogh: Prediction of signal peptides and signal anchors by a hidden Markov model. In *Proceedings of the Sixth International Conference on Intelligent Systems for Molecular Biology (ISMB 6)*, AAAI Press, Menlo Park, California, pp. 122--130 (1998).

<http://www.cbs.dtu.dk/cgi-bin/nph-webface?jobid=signalp,3F94DCB9006C20D0&opt=none> 21-Oct-0:



Figure 3



data

```
>#
Prediction: Signal peptide
Signal peptide probability: 1.000
Signal anchor probability: 0.000
Max cleavage site probability: 0.981 between pos. 24 and 25
```

gnuplot script for making the plot(s)

When using results from this server, please cite:

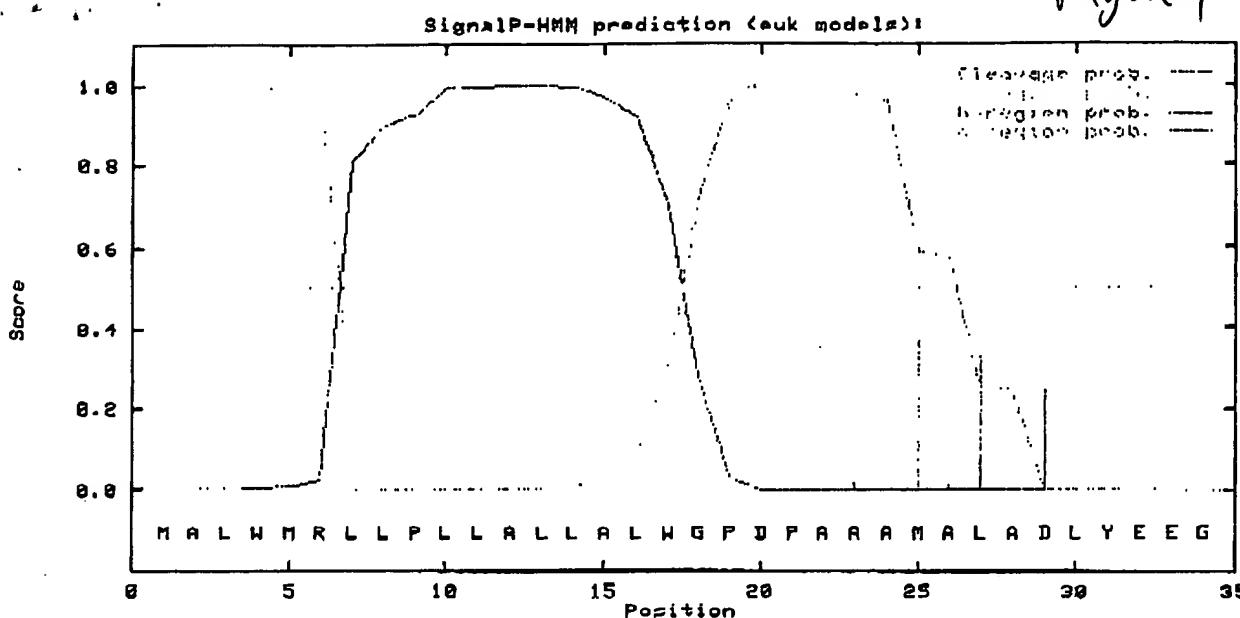
- Henrik Nielsen, Jacob Engelbrecht, Søren Brunak and Gunnar von Heijne: Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites. *Protein Engineering*, 10, 1-6 (1997).

If you specifically use the SignalP-HMM output, please also cite:

- Henrik Nielsen and Anders Krogh: Prediction of signal peptides and signal anchors by a hidden Markov model. In *Proceedings of the Sixth International Conference on Intelligent Systems for Molecular Biology (ISMB 6)*, AAAI Press, Menlo Park, California, pp. 122--130 (1998).

IL¹ β
INSVLHSP

Figure 4



Insulin sp ↑ ↑ ↑ cIL-1 α -II

data

>
Prediction: Signal peptide
Signal peptide probability: 1.000
Signal anchor probability: 0.000
Max cleavage site probability: 0.375 between pos. 24 and 25

gnuplot script for making the plot(s)

When using results from this server, please cite:

- Henrik Nielsen, Jacob Engelbrecht, Søren Brunak and Gunnar von Heijne: Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites. *Protein Engineering*, 10, 1-6 (1997).

If you specifically use the SignalP-HMM output, please also cite:

- Henrik Nielsen and Anders Krogh: Prediction of signal peptides and signal anchors by a hidden Markov model. In *Proceedings of the Sixth International Conference on Intelligent Systems for Molecular Biology (ISMB 6)*, AAAI Press, Menlo Park, California, pp. 122-130 (1998).

IL-1 α
in s/uN sp

<http://www.cbs.dtu.dk/cgi-bin/nph-webface?jobid=signalp,3F36468E022AAED6&opt=none> 8/10/2001

